

2590
0429
#8



OICE

RAW SEQUENCE LISTING

DATE: 05/02/2002

PATENT APPLICATION: US/09/982,543A

TIME: 17:23:22

Input Set : A:\CIBT-P04-523 Sequence Listing.txt

Output Set: N:\CRF3\05022002\I982543A.raw

p.6

ENTERED

```

4 <110> APPLICANT: Dijke, P.
5      Miyazano, K.
6      Sampath, K.
7      Heldin, C.
9 <120> TITLE OF INVENTION: MORPHOGENIC PROTEIN-SPECIFIC CELL SURFACE RECEPTORS AND USES
10     THEREFOR
12 <130> FILE REFERENCE: CIBT-P04-543
14 <140> CURRENT APPLICATION NUMBER: 09/982,543A
15 <141> CURRENT FILING DATE: 2001-10-18
17 <150> PRIOR APPLICATION NUMBER: 08/448,371
18 <151> PRIOR FILING DATE: 1995-06-02
20 <160> NUMBER OF SEQ ID NOS: 15
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1509
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(1509)
32 <223> OTHER INFORMATION:
34 <400> SEQUENCE: 1
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36 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
37 1          5          10          15
39 ttg gtg acc cag gga gac cct gtg aag ccg tct cgg ggc ccg ctg gtg      96
40 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
41          20          25          30
43 acc tgc acg tgt gag agc cca cat tgc aag ggg cct acc tgc cgg ggg      144
44 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
45          35          40          45
47 gcc tgg tgc aca gta gtg ctg gtg cgg gag gag ggg agg cac ccc cag      192
48 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
49          50          55          60
51 gaa cat cgg ggc tgc ggg aac ttg cac agg gag ctc tgc agg ggg cgc      240
52 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
53 65          70          75          80
55 ccc acc gag ttc gtc aac cac tac tgc tgc gac agc cac ctc tgc aac      288
56 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
57          85          90          95
59 cac aac gtg tcc ctg gtg ctg gag gcc acc caa cct cct tcg gag cag      336
60 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
61          100          105          110

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63	ccg gga aca gat ggc cag ctg gcc ctg atc ctg ggc ccc gtg ctg gcc	384
64	Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala	
65	115 120 125	
67	ttg ctg gcc ctg gtg gcc ctg ggt gtc ctg ggc ctg tgg cat gtc cga	432
68	Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg	
69	130 135 140	
71	cgg agg cag gag aag cag cgt ggc ctg cac agc gag ctg gga gag tcc	480
72	Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser	
73	145 150 155 160	
75	agt ctc atc ctg aaa gca tct gag cag ggc gac acg atg ttg ggg gac	528
76	Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp	
77	165 170 175	
79	ctc ctg gac agt gac tgc acc aca ggg agt ggc tca ggg ctc ccc ttc	576
80	Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe	
81	180 185 190	
83	ctg gtg cag agg aca gtg gca cgg cag gtt gcc ttg gtg gag tgt gtg	624
84	Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val	
85	195 200 205	
87	gga aaa ggc cgc tat ggc gaa gtg tgg cgg ggc ttg tgg cac ggt gag	672
88	Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu	
89	210 215 220	
91	agt gtg gcc gtc aag atc ttc tcc tcc agg gat gaa cag tcc tgg ttc	720
92	Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe	
93	225 230 235 240	
95	cgg gag act gag atc tat aac aca gta ttg ctc aga cac gac aac atc	768
96	Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Leu Arg His Asp Asn Ile	
97	245 250 255	
99	cta ggc ttc atc gcc tca gac atg acc tcc cgc aac tcc agc acg cag	816
100	Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln	
101	260 265 270	
103	ctg tgg ctc atc acg cac tac cac gag cac ggc tcc ctc tac gac ttt	864
104	Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe	
105	275 280 285	
107	ctg cag aga cag acg ctg gag ccc cat ctg gct ctg agg cta gct gtg	912
108	Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val	
109	290 295 300	
111	tcc gcg gca tgc ggc ctg gcg cac ctg cac gtg gag atc ttc ggt aca	960
112	Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr	
113	305 310 315 320	
115	cag ggc aaa cca gcc att gcc cac cgc gac ttc aag agc cgc aat gtg	1008
116	Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val	
117	325 330 335	
119	ctg gtc aag agc aac ctg cag tgt tgc atc gcc gac ctg ggc ctg gct	1056
120	Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala	
121	340 345 350	
123	gtg atg cac tca cag ggc agc gat tac ctg gac atc ggc aac aac ccg	1104
124	Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro	
125	355 360 365	
127	aga gtg ggc acc aag cgg tac atg gca ccc gag gtg ctg gac gag cag	1152

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128 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
129      370      375      380
131 atc cgc acg gac tgc ttt gag tcc tac aag tgg act gac atc tgg gcc      1200
132 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
133 385      390      395      400
135 ttt ggc ctg gtg ctg tgg gag att gcc cgc cgg acc atc gtg aat ggc      1248
136 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
137      405      410      415
139 atc gtg gag gac tat aga cca ccc ttc tat gat gtg gtg ccc aat gac      1296
140 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
141      420      425      430
143 ccc agc ttt gag gac atg aag aag gtg gtg tgt gtg gat cag cag acc      1344
144 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
145      435      440      445
147 ccc acc atc cct aac cgg ctg gct gca gac ccg gtc ctc tca ggc cta      1392
148 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
149      450      455      460
151 gct cag atg atg cgg gag tgc tgg tac cca aac ccc tct gcc cga ctc      1440
152 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
153 465      470      475      480
155 acc gcg ctg cgg atc aag aag aca cta caa aaa att agc aac agt cca      1488
156 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
157      485      490      495
159 gag aag cct aaa gtg att caa      1509
160 Glu Lys Pro Lys Val Ile Gln
161      500
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 503
165 <212> TYPE: PRT
166 <213> ORGANISM: Homo sapiens
168 <400> SEQUENCE: 2
169 Met Thr Leu Gly Ser Pro Arg Lys Gly Leu Leu Met Leu Leu Met Ala
170 1      5      10      15
172 Leu Val Thr Gln Gly Asp Pro Val Lys Pro Ser Arg Gly Pro Leu Val
173      20      25      30
175 Thr Cys Thr Cys Glu Ser Pro His Cys Lys Gly Pro Thr Cys Arg Gly
176      35      40      45
178 Ala Trp Cys Thr Val Val Leu Val Arg Glu Glu Gly Arg His Pro Gln
179      50      55      60
181 Glu His Arg Gly Cys Gly Asn Leu His Arg Glu Leu Cys Arg Gly Arg
182 65      70      75      80
184 Pro Thr Glu Phe Val Asn His Tyr Cys Cys Asp Ser His Leu Cys Asn
185      85      90      95
187 His Asn Val Ser Leu Val Leu Glu Ala Thr Gln Pro Pro Ser Glu Gln
188      100      105      110
190 Pro Gly Thr Asp Gly Gln Leu Ala Leu Ile Leu Gly Pro Val Leu Ala
191      115      120      125
193 Leu Leu Ala Leu Val Ala Leu Gly Val Leu Gly Leu Trp His Val Arg
194      130      135      140

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196 Arg Arg Gln Glu Lys Gln Arg Gly Leu His Ser Glu Leu Gly Glu Ser
197 145 150 155 160
199 Ser Leu Ile Leu Lys Ala Ser Glu Gln Gly Asp Thr Met Leu Gly Asp
200 165 170 175
202 Leu Leu Asp Ser Asp Cys Thr Thr Gly Ser Gly Ser Gly Leu Pro Phe
203 180 185 190
205 Leu Val Gln Arg Thr Val Ala Arg Gln Val Ala Leu Val Glu Cys Val
206 195 200 205
208 Gly Lys Gly Arg Tyr Gly Glu Val Trp Arg Gly Leu Trp His Gly Glu
209 210 215 220
211 Ser Val Ala Val Lys Ile Phe Ser Ser Arg Asp Glu Gln Ser Trp Phe
212 225 230 235 240
214 Arg Glu Thr Glu Ile Tyr Asn Thr Val Leu Arg His Asp Asn Ile
215 245 250 255
217 Leu Gly Phe Ile Ala Ser Asp Met Thr Ser Arg Asn Ser Ser Thr Gln
218 260 265 270
220 Leu Trp Leu Ile Thr His Tyr His Glu His Gly Ser Leu Tyr Asp Phe
221 275 280 285
223 Leu Gln Arg Gln Thr Leu Glu Pro His Leu Ala Leu Arg Leu Ala Val
224 290 295 300
226 Ser Ala Ala Cys Gly Leu Ala His Leu His Val Glu Ile Phe Gly Thr
227 305 310 315 320
229 Gln Gly Lys Pro Ala Ile Ala His Arg Asp Phe Lys Ser Arg Asn Val
230 325 330 335
232 Leu Val Lys Ser Asn Leu Gln Cys Cys Ile Ala Asp Leu Gly Leu Ala
233 340 345 350
235 Val Met His Ser Gln Gly Ser Asp Tyr Leu Asp Ile Gly Asn Asn Pro
236 355 360 365
238 Arg Val Gly Thr Lys Arg Tyr Met Ala Pro Glu Val Leu Asp Glu Gln
239 370 375 380
241 Ile Arg Thr Asp Cys Phe Glu Ser Tyr Lys Trp Thr Asp Ile Trp Ala
242 385 390 395 400
244 Phe Gly Leu Val Leu Trp Glu Ile Ala Arg Arg Thr Ile Val Asn Gly
245 405 410 415
247 Ile Val Glu Asp Tyr Arg Pro Pro Phe Tyr Asp Val Val Pro Asn Asp
248 420 425 430
250 Pro Ser Phe Glu Asp Met Lys Lys Val Val Cys Val Asp Gln Gln Thr
251 435 440 445
253 Pro Thr Ile Pro Asn Arg Leu Ala Ala Asp Pro Val Leu Ser Gly Leu
254 450 455 460
256 Ala Gln Met Met Arg Glu Cys Trp Tyr Pro Asn Pro Ser Ala Arg Leu
257 465 470 475 480
259 Thr Ala Leu Arg Ile Lys Lys Thr Leu Gln Lys Ile Ser Asn Ser Pro
260 485 490 495
262 Glu Lys Pro Lys Val Ile Gln
263 500
265 <210> SEQ ID NO: 3
266 <211> LENGTH: 2724
267 <212> TYPE: DNA

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268 <213> ORGANISM: Homo sapiens
270 <220> FEATURE:
271 <221> NAME/KEY: CDS
272 <222> LOCATION: (104)..(1633)
273 <223> OTHER INFORMATION:
275 <400> SEQUENCE: 3
276 ctccgagtac cccagtgacc agagtgagag aagctctgaa cgaggggcacg cggcttgaag      60
277 gactgtgggc agatgtgacc aagagcctgc attaagttgt aca atg gta gat gga      115
278                                     Met Val Asp Gly
279                                     1
280
282 gtg atg att ctt cct gtg ctt atc atg att gct ctc ccc tcc cct agt      163
283 Val Met Ile Leu Pro Val Leu Ile Met Ile Ala Leu Pro Ser Pro Ser
284 5                                     10                                     15                                     20
286 atg gaa gat gag aag ccc aag gtc aac ccc aaa ctc tac atg tgt gtg      211
287 Met Glu Asp Glu Lys Pro Lys Val Asn Pro Lys Leu Tyr Met Cys Val
288                                     25                                     30                                     35
290 tgt gaa ggt ctc tcc tgc ggt aat gag gac cac tgt gaa ggc cag cag      259
291 Cys Glu Gly Leu Ser Cys Gly Asn Glu Asp His Cys Glu Gly Gln Gln
292                                     40                                     45                                     50
294 tgc ttt tcc tca ctg agc atc aac gat ggc ttc cac gtc tac cag aaa      307
295 Cys Phe Ser Ser Leu Ser Ile Asn Asp Gly Phe His Val Tyr Gln Lys
296                                     55                                     60                                     65
298 ggc tgc ttc cag gtt tat gag cag gga aag atg acc tgt aag acc ccg      355
299 Gly Cys Phe Gln Val Tyr Glu Gln Gly Lys Met Thr Cys Lys Thr Pro
300                                     70                                     75                                     80
302 ccg tcc cct ggc caa gct gtg gag tgc tgc caa ggg gac tgg tgt aac      403
303 Pro Ser Pro Gly Gln Ala Val Glu Cys Cys Gln Gly Asp Trp Cys Asn
304 85                                     90                                     95                                     100
306 agg aac atc acg gcc cag ctg ccc act aaa gga aaa tcc ttc cct gga      451
307 Arg Asn Ile Thr Ala Gln Leu Pro Thr Lys Gly Lys Ser Phe Pro Gly
308                                     105                                     110                                     115
310 aca cag aat ttc cac ttg gag gtt ggc ctc att att ctc tct gta gtg      499
311 Thr Gln Asn Phe His Leu Glu Val Gly Leu Ile Ile Leu Ser Val Val
312                                     120                                     125                                     130
314 ttc gca gta tgt ctt tta gcc tgc ctg ctg gga gtt gct ctc cga aaa      547
315 Phe Ala Val Cys Leu Leu Ala Cys Leu Leu Gly Val Ala Leu Arg Lys
316                                     135                                     140                                     145
318 ttt aaa agg cgc aac caa gaa cgc ctc aat ccc cga gac gtg gag tat      595
319 Phe Lys Arg Arg Asn Gln Glu Arg Leu Asn Pro Arg Asp Val Glu Tyr
320                                     150                                     155                                     160
322 ggc act atc gaa ggg ctc atc acc acc aat gtt gga gac agc act tta      643
323 Gly Thr Ile Glu Gly Leu Ile Thr Thr Asn Val Gly Asp Ser Thr Leu
324 165                                     170                                     175                                     180
326 gca gat tta ttg gat cat tcg tgt aca tca gga agt ggc tct ggt ctt      691
327 Ala Asp Leu Leu Asp His Ser Cys Thr Ser Gly Ser Gly Ser Gly Leu
328                                     185                                     190                                     195
330 cct ttt ctg gta caa aga aca gtg gct cgc cag att aca ctg ttg gag      739
331 Pro Phe Leu Val Gln Arg Thr Val Ala Arg Gln Ile Thr Leu Leu Glu
332                                     200                                     205                                     210

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 2,3,9,11,16,19,23,26,35,39,41,50,52,56,57,58,60,61,65,71

Seq#:11; Xaa Pos. 73,75,80,82,84,87,89,91,97

Seq#:12; N Pos. 20